

# Alignment 1

RESULT 11  
 ID R15141 standard; Protein; 344 AA.  
 AC R15141;  
 DT 24-FEB-1992 (first entry)  
 DE RecA.  
 KW Recombinant repair; amplification.  
 OS Aquaspirillum magnetotacticum.  
 PN WO9117267-A.  
 PD 14-NOV-1991.  
 PF 17-APR-1991; U02626.  
 PR 07-MAY-1990; US-520321.

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PA (STRI ) SRI INTERNATIONAL.  
 PI Zarling DA, Sena EP, Green CJ;  
 DR WPI; 91-353786/48.  
 DR N-PSDB; Q14781.  
 PT Amplification of target DNA sequences - using primers, RecA  
 protein, ATP-gamma-S, dNTPs and DNA polymerase.  
 PS Example 10; Fig 13; 52pp; English.  
 CC DNA encoding the sequence, plus a further 800 bp of uncharacterised  
 CC genomic DNA, was used as a probe to identify and clone the Thermus  
 CC aquaticus RecA gene. The heat stable RecA protein encoded by the T.  
 CC aquaticus gene can be used in a new method for the amplification of  
 CC target DNA sequences. The RecA protein strongly facilitates hybridis-  
 CC ation of the primers to the DNA and prepn. of the primer-target com-  
 CC plex topologically for extension by the polymerase. ATP-gamma-S acts  
 CC as a cofactor in strand transfer. The reaction may be carried out at a  
 CC temp. above 50 deg. C and below the temp. required for thermal dis-  
 CC sociation of the target strands and primers. The RecA coated primers  
 CC may be useful as probes in diagnostic systems.  
 SQ Sequence 344 AA;

Query Match 70.7%; Score 99; DB 1; Length 344;  
 Best Local Similarity 46.2%; Pred. No. 5.22e-02;  
 Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 38 VSTRILGLDVALGIGGVPGGRIVEY 63  
 :||| :|||:| :| :||:|  
 Qy 1 ISTXSLSLDIALXXXXLPMXRIVEIY 26

## Alignment 2

sp|P95526|RECA\_PASMU RECA PROTEIN >gi|1772591|emb|CAA67699.1| (X99324)  
RecA protein  
[Pasteurella multocida]  
Length = 354

Score = 49.2 bits (115), Expect = 5e-06  
Identities = 22/26 (84%), Positives = 25/26 (95%)

Query: 1 ISTGSLSLDIALGAGGLPMGRIVEIY 26  
+STGSLSLD+ALG GGLPMGRIVEI+  
Sbjct: 41 VSTGSLSLDVALGIGGLPMGRIVEIF 66

↑

↑

1: P95526. RECA PROTEIN...[gi:3219853]  
 LOCUS RECA\_PASMU 354 aa BCT 15-FEB-2000 A2 4/27  
 DEFINITION RECA\_PROTEIN.  
 ACCESSION P95526  
 PID g3219853  
 VERSION P95526 GI:3219853  
 DBSOURCE swissprot: locus RECA\_PASMU, accession P95526;  
 class: standard.  
 → created: Jul 15, 1998.  
 sequence updated: Jul 15, 1998.  
 annotation updated: Feb 15, 2000.  
 xrefs: gi: 1772590, gi: 1772591  
 xrefs (non-sequence databases): HSSP P03017, PFAM PF00154, PROSITE  
 PS00321  
 KEYWORDS DNA damage; DNA recombination; SOS response; ATP-binding;  
 DNA-binding.  
 SOURCE Pasteurella multocida.  
 ORGANISM Pasteurella multocida  
 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 Pasteurella.  
 REFERENCE 1 (residues 1 to 354)  
 AUTHORS Barbe Garcia, J.  
 TITLE Direct Submission  
 → JOURNAL Submitted (??-JUL-1996) to the EMBL/GenBank/DDBJ databases  
 REMARK SEQUENCE FROM N.A.  
 STRAIN=2,5  
 COMMENT

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 This SWISS-PROT entry is copyright. It is produced through a  
 collaboration between the Swiss Institute of Bioinformatics and  
 the EMBL outstation - the European Bioinformatics Institute.  
 The original entry is available from <http://www.expasy.ch/sprot>  
 and <http://www.ebi.ac.uk/sprot>  
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[FUNCTION] RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE  
 PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF  
 SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT  
 HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH  
 LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC  
 CLEAVAGE.

[SIMILARITY] BELONGS TO THE RECA FAMILY.

FEATURES Location/Qualifiers  
 source 1..354  
 /organism="Pasteurella multocida"  
 /db\_xref="taxon:747"  
 Protein 1..354  
 /product="RECA PROTEIN"  
 Site 67..74  
 /site\_type="np-binding"  
 /note="ATP (POTENTIAL)."

# ORIGIN

1 matkeeknka laaalgqiek qfgkgsimkl gdtqaldvea vstgslsldv algigglpmg  
 61 riveifgpes sgkttltlsv iaqaqkegkt cafidaehal dpiyaaklgv nvnellvsqp  
 121 dngeqaleic dalvrsgavd viivdsvaal tpkaeiegem gdshmgqlqar lmsqalrklt  
 181 gqiknsnclv vfinqirmki gvmfgnpett tggnaikfya svrldirrtg aikegeevig  
 241 netrvkvvkn kvaapfrqvd fqilygggis ktgelielgv khklvdkaga wyayngekig  
 301 qgkanamkwI eehpeealal etklrnella npekvlaadi aeknesstgl eady

//

*Alignment 3*

gb|AAC16335.1| (AF062380) Dmcl homolog [Leishmania major]  
Length = 364

Score = 28.9 bits (63), Expect = 6.6  
Identities = 13/26 (50%), Positives = 16/26 (61%)

Query: 1 ISTGSLSLDIALGAGGLPMGRIVEIY 26  
ISTGS +LD LG GG+ I E +  
Sbjct: 126 ISTGSTALDQLLGGGGIESRSITEAF 151

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☐ 1 : AAC16335 . (AF062380) Dmc1 ho...[gi:3132711]

[Related Sequences](#), [Nucleotide](#)

LOCUS AAC16335 364 aa INV 14-MAY-1998  
DEFINITION Dmc1 homolog [Leishmania major].  
ACCESSION AAC16335  
PID g3132711  
VERSION AAC16335.1 GI:3132711  
DBSOURCE locus AF062380 accession AF062380.1  
KEYWORDS .  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Leishmania.  
REFERENCE 1 (residues 1 to 364)  
AUTHORS McKean, P.G. and Benson, F.E.  
TITLE Direct Submission  
JOURNAL Submitted (30-APR-1998) Biochemistry, Imperial College of Science,  
Technology and Medicine, London, Herts. SW7 2AZ, UK  
COMMENT Method: conceptual translation supplied by author.  
FEATURES  
Location/Qualifiers  
source 1..364  
/organism="Leishmania major"  
/strain="Friedlin"  
/db\_xref="taxon:5664"  
/chromosome="35"  
Protein 1..364  
/product="Dmc1 homolog"  
CDS 1..364  
/gene="DMC1"  
/coded\_by="AF062380.1:1..1095"  
ORIGIN  
1 mqqqqqqqqrq hsshfaeerv gdrgaafaep qplhnsvtge aagqsllve rlaehgigaa  
61 ditklkqagi ftvpgvqmqc rkdliqikgl seakvdkiie aarrvsevgf itgssclqqr  
121 stllristgs talldqllggg giesrsitea fgeftrgtktq ightlcvtcq lplemggng  
181 kavyvdtegt frperirpia erfmdsnsv ldnilvaray theqhahlls mvaakmaedq  
241 fsllvdsit alfrvdfsgg gelaerqqkl akmlsqliki aeefniavyi tnqvvsdpqg  
301 asmfvadpkk pvgghilaha sttrlslrkg rgdqrvcikf dspslpelec vysiseqgii  
361 dave  
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Display	<input type="text" value="GenPept"/>	<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>
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Revised: January 10, 2000.

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*Alignment 4*

pir||RQBCAT recombination protein recA - Thiobacillus ferrooxidans  
Length = 346

Score = 44.9 bits (104), Expect = 1e-04  
Identities = 21/26 (80%), Positives = 22/26 (83%)

Query: 1 ISTGSLMLDNALGAGGLPMGRIVEIY 26  
STGSL LD ALG GGLP GR+VEIY  
Sbjct: 40 YSTGSLGLDLALGVGGLPRGRVVEIY 65  
↑



Entrez  
Protein

PubMed	Nucleotide	Protein	Genome	Structure	PopSet
Search <input type="text" value="Protein"/> for <input type="text"/>					
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<input type="button" value="Limits"/>		<input type="button" value="Preview/Index"/>		<input type="button" value="History"/>	
<input type="button" value="Clipboard"/>					

Display <input type="text" value="GenPept"/>	<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>
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**1 : RQBCAT . recombination prot...[gi:72986]**

PubMed, Related Sequences

LOCUS RQBCAT 346 aa BCT 05-MAR-1999  
 DEFINITION recombination protein recA - Thiobacillus ferrooxidans.  
 ACCESSION RQBCAT  
 PID g72986  
 VERSION RQBCAT GI:72986  
 DBSOURCE pir: locus RQBCAT;  
 summary: #length 346 #molecular-weight 37096 #checksum 5119;  
 genetic: #gene recA;  
 superfamily: recombination protein recA;  
 PIR dates: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Mar-1999.

KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS response.

SOURCE Thiobacillus ferrooxidans.

ORGANISM Thiobacillus ferrooxidans

Bacteria; Proteobacteria; gamma subdivision.

REFERENCE 1 (residues 1 to 346)

AUTHORS Ramesar,R.S., Abratt,V., Woods,D.R. and Rawlings,D.E.

→ TITLE Nucleotide sequence and expression of a cloned Thiobacillus ferrooxidans recA gene in Escherichia coli

→ JOURNAL Gene 78 (1), 1-8 (1989)

MEDLINE 89357486

FEATURES Location/Qualifiers  
 source 1..346  
 /organism="Thiobacillus ferrooxidans"  
 /db\_xref="taxon:920"  
 Protein 1..346  
 /product="recombination protein recA"  
 /note="recombinase A"  
 Region 66..73  
 /region\_name="region"  
 /note="nucleotide-binding motif A (P-loop)"  
 Site 72  
 /site\_type="binding"  
 /note="ATP (Lys)"  
 Region 140..145  
 /region\_name="region"  
 /note="nucleotide-binding motif B"

ORIGIN

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1 mdeqrskgls aalsqidkqf gkgavmrlgd hnaikdievy stgslgldla lgvgglprgr
61 vveiygpess gkttlthai ascqaaggt aafidaehald pgyahklgvd lenllisqpd
121 tgeqaleiad mlvrsgavdl ividsvaalt pkaeiegemg dshvgkqarl msqalrnlt
181 nisrsntlvi finqirmkig vmygspett ggnalkfyas vrlidirriga ikksdevvgn
241 dtrvkvvknk vappfreaef aiyygegiss lseldvlgvl fdiveksgaw ysyqghrigq
301 gkdnarqylk vhpelaanie qrraaaaagh plafaeaves pqrzas

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